AMENDMENTS TO THE SPECIFICATION

Please replace paragraph 62 with the following paragraph:

--FIG. 19: View of amino acid residue positions on Lep d 2: K6, S22, R30, K76, K81, V114 that are selected in example 2A as possible target positions for the introduction of secondary mutations. ABCD show molecular surfaces of Lep d 2 (accession no S66499) modeled at SWISS-MODEL ~~http://www.expasy.org/swissmod/SWISS-MODEL.html~~ using pdb entry 1ktj as template. A=front view, B=Turn 1 (front view turned 90° out of plane around the horizontal axes), C=Turn 2 (front view turned 180° out of plane around the horizontal axes), D=Turn 3 (front view turned 270° out of plane around the horizontal axes). Grey color shows α-carbon backbone atoms and side chain atoms on amino acid residues that are identical or homologous to Der p 2 specific amino acid residues in corresponding amino acid positions. White color shows amino acid residues that are specific for Lep d 2 (accession no S66499). Black color shows amino acid residues on Lep d 2 that in example 2A are selected as possible targets for the introduction of secondary mutations.--

Please replace paragraph 63 with the following paragraph:

-- FIG. 20: View of amino acid residue positions on Lep d 2: D17, S19, Q32, K33, T35, N88, T92, A95, that are selected in example 2A as possible target positions for the introduction of primary mutations. ABCD show molecular surfaces of Lep d 2 (accession no S66499) modeled at SWISS-MODEL ~~http://www.expasy.org/swissmod/SWISS-MODEL.html~~ using pdb entry 1 ktj as template. A=front view, B=Turn 1 (front view turned 90° out of plane around the horizontal axes), C=Turn 2 (front view turned 180° out of plane around the horizontal axes), D=Turn 3 (front view turned 2700 out of plane around the horizontal axes). Grey color shows .alpha.-carbon backbone atoms and side chain atoms on amino acid residues that are identical or homologous to Der p 2 specific amino acid residues in corresponding amino acid positions on Der p 2 (pdb entry 1ktj). White color shows amino acid residues that are specific for Lep d 2 (accession no s66499). Black color shows amino acid residues on Lep d 2 that in example 2A are selected as possible targets for the introduction of primary mutations. --

Please replace paragraph 67 with the following paragraph:

-- AJ272216) modeled at <u>SWISS-MODEL</u> ~~http://www.expasy.org/swissmod/SWISS-MODEL.htm-l~~ using pdb entry 1 ktj as template. A=front view, B=Turn 1 (front view turned 90° out of plane around the horizontal axes), C=Turn 2 (front view turned 180° out of plane around the horizontal axes), D=Turn 3 (front view turned 270° out of plane around the horizontal axes). Grey color shows .alpha.-carbon backbone atoms and side chain atoms on amino acid residues that are identical or homologous to Der p 2 specific amino acid residues in corresponding amino acid positions on Der p 2 (pdb entry 1ktj). White color shows amino acid residues that are specific for Gly d 2 (accession no. AJ272216). Black color shows amino acid residues on Gly d 2 that in example 4 are selected as possible targets for the introduction of secondary mutations. --

Please replace paragraph 68 with the following paragraph:

-- FIG. 24: View of amino acid residue positions on Gly d 2 that are selected in example 4 as possible target positions for the introduction of primary mutations. ABCD show molecular surfaces of Gly d 2 (accession no. AJ272216) modeled at <u>SWISS-MODEL</u> ~~http://www.expasy.org/swissmod/SWISS-MODEL.html~~ using pdb entry 1 ktj as template. A=front view, B=Turn 1 (front view turned 90° out of plane around the horizontal axes), C=Turn 2 (front view turned 180° out of plane around the horizontal axes), D=Turn 3 (front view turned 270° out of plane around the horizontal axes). Grey color shows .alpha.-carbon backbone atoms and side chain atoms on amino acid residues that are identical or homologous to Der p 2 specific amino acid residues in corresponding amino acid positions on Der p 2 (pdb entry 1ktj). White color show amino acid residues that are specific for Gly d 2 (accession no. AJ272216). Black color shows amino acid residues on Gly d 2 that in example 4 are selected as possible targets for the introduction of primary mutations. --

Please replace paragraphs 251-252 with the following paragraphs:

-- CD spectra recorded in the wavelength range 260 nm to at least 184 nm were deconvoluted by the program CDNN.÷

~~www.bioinformatik.biochemtech.uni-halle.de/cdnn~~ --